



RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/1767764
Source: OIPE
Date Processed by STIC: 09/21/01

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:
1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE
APPLICANT, WITH A NOTICE TO COMPLY or,
2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A
NOTICE TO COMPLY
FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.
PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)
PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER
VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND
TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:
<http://www.uspto.gov/web/offices/pac/checker>

Raw Sequence Listing Error Summary

<u>ERROR DETECTED</u>	<u>SUGGESTED CORRECTION</u>	SERIAL NUMBER: <u>09/767764</u>
ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PT		
1 <input type="checkbox"/> Wrapped Nucleic Wrapped Aminos	The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."	
2 <input type="checkbox"/> Invalid Line Length	The rules require that a line not exceed 72 characters in length. This includes white spaces.	
3 <input checked="" type="checkbox"/> Misaligned Amino Numbering	The numbering under each 5' amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead. nucleotide	
4 <input type="checkbox"/> Non-ASCII	The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.	
5 <input type="checkbox"/> Variable Length	Sequence(s) _____ contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.	
6 <input type="checkbox"/> PatentIn 2.0 "bug"	A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.	
7 <input type="checkbox"/> Skipped Sequences (OLD RULES)	Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading) (xi) SEQUENCE DESCRIPTION: SEQ ID NO:X: (insert SEQ ID.NO where "X" is shown) This sequence is intentionally skipped	
8 <input type="checkbox"/> Skipped Sequences (NEW RULES)	Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences. Sequence(s) _____ missing. If Intentional, please insert the following lines for each skipped sequence <210> sequence id number <400> sequence id number 000	
9 <input type="checkbox"/> Use of n's or Xaa's (NEW RULES)	Use of n's and/or Xaa's have been detected in the Sequence Listing. Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present. In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents	
10 <input type="checkbox"/> Invalid <213> Response	Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or Artificial Sequence	
11 <input type="checkbox"/> Use of <220>	Sequence(s) _____ missing the <220> "Feature" and associated numeric identifiers and responses Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section. (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)	
12 <input type="checkbox"/> PatentIn 2.0 "bug"	Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.	
13 <input type="checkbox"/> Misuse of n	n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide.	

OIPE

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/767,764

DATE: 09/21/2001
TIME: 17:34:54

Input Set : A:\SeqList.txt
Output Set: N:\CRF3\09212001\I767764.raw

3 <110> APPLICANT: Church, George
5 <120> TITLE OF INVENTION: Method Of Making Protein Arrays
7 <130> FILE REFERENCE: 10498-00009
C--> 9 <140> CURRENT APPLICATION NUMBER: US/09/767,764
C--> 9 <141> CURRENT FILING DATE: 2001-01-23
9 <150> PRIOR APPLICATION NUMBER: US 09/522,732
11 <151> PRIOR FILING DATE: 2000-03-10
13 <160> NUMBER OF SEQ ID NOS: 21
15 <170> SOFTWARE: PatentIn version 3.0

Does Not Comply
Corrected Diskette Needed

ERRORED SEQUENCES

17 <210> SEQ ID NO: 1
18 <211> LENGTH: 24
19 <212> TYPE: DNA
20 <213> ORGANISM: Bacteriophage T7
22 <400> SEQUENCE: 1
E--> 23 taatacgact cacta ta (17) invalid alignment - Invalid nucleotide numbering
E--> 24 (24) invalid alignment - Invalid nucleotide numbering
27 <210> SEQ ID NO: 2
28 <211> LENGTH: 24
29 <212> TYPE: DNA
30 <213> ORGANISM: Artificial Sequence
32 <220> FEATURE:
33 <221> NAME/KEY: misc_feature
34 <222> LOCATION: ()..()
35 <223> OTHER INFORMATION: Amplification primer.
37 <400> SEQUENCE: 2
E--> 38 ccaactacgccc tccgcctttcc tctc (24) invalid alignment - Invalid nucleotide numbering
39 (24) invalid alignment - Invalid nucleotide numbering
42 <210> SEQ ID NO: 3
43 <211> LENGTH: 23
44 <212> TYPE: DNA
45 <213> ORGANISM: Artificial Sequence
48 <220> FEATURE:
49 <221> NAME/KEY: misc_feature
50 <222> LOCATION: ()..()
51 <223> OTHER INFORMATION: Amplification primer.
53 <400> SEQUENCE: 3
E--> 54 ctggccccggg ttcccttcattc tct (23) invalid alignment - Invalid nucleotide numbering
55 (23) invalid alignment - Invalid nucleotide numbering
58 <210> SEQ ID NO: 4
59 <211> LENGTH: 24
60 <212> TYPE: DNA
61 <213> ORGANISM: Artificial Sequence
63 <220> FEATURE:

See Error Summary Sheet
See pages 1 and 2

invalid alignment - Invalid nucleotide numbering

Global Errors

invalid alignment - Invalid nucleotide numbering

invalid alignment - Invalid nucleotide numbering

invalid nucleotide numbering MT

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Input Set : A:\SeqList.txt
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64 <221> NAME/KEY: misc_feature
 65 <222> LOCATION: ()..()
 66 <223> OTHER INFORMATION: Amplification primer.
 68 <220> FEATURE:
 W--> 69 <221> NAME/KEY: misc_feature<222> (1)..(1)
 70 <223> OTHER INFORMATION: 5' end modified with acrydite.
 E--> 73 ccactacgcc tccgcttcc tctc (24) should appear at the end of the nucleotide string.
 74 24
 77 <210> SEQ ID NO: 5
 78 <211> LENGTH: 24
 79 <212> TYPE: DNA
 80 <213> ORGANISM: Artificial Sequence
 82 <220> FEATURE:
 83 <221> NAME/KEY: misc_feature
 84 <222> LOCATION: ()..()
 85 <223> OTHER INFORMATION: Amplification primer.
 87 <400> SEQUENCE: 5
 E--> 88 gggcggaaagc ttgaaggagg tatt invalid nucleotide numbering
 89 (24) 6
 92 <210> SEQ ID NO: 6
 93 <211> LENGTH: 23
 94 <212> TYPE: DNA
 95 <213> ORGANISM: Artificial Sequence
 97 <220> FEATURE:
 98 <221> NAME/KEY: misc_feature
 99 <222> LOCATION: ()..()
 100 <223> OTHER INFORMATION: Amplification primer.
 102 <400> SEQUENCE: 6
 E--> 103 gcccggtctc gagcgctgt tta numbering should appear at the end of the nucleotide string.
 104 (23) 7
 107 <210> SEQ ID NO: 7
 108 <211> LENGTH: 24
 109 <212> TYPE: DNA
 110 <213> ORGANISM: Artificial Sequence
 112 <220> FEATURE:
 113 <221> NAME/KEY: misc_feature
 114 <222> LOCATION: ()..()
 115 <223> OTHER INFORMATION: Amplification primer.
 117 <220> FEATURE:
 118 <221> NAME/KEY: misc_feature
 119 <222> LOCATION: (1)..(1)
 120 <223> OTHER INFORMATION: 5' end modified with acrydite.
 122 <400> SEQUENCE: 7
 E--> 123 gggcggaaagc ttgaaggagg tatt
 124 (24) 8
 127 <210> SEQ ID NO: 8
 128 <211> LENGTH: 47
 129 <212> TYPE: DNA

RAW SEQUENCE LISTING
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Input Set : A:\SeqList.txt
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130 <213> ORGANISM: Artificial Sequence
132 <220> FEATURE:
133 <221> NAME/KEY: misc_feature
134 <222> LOCATION: ()..()
135 <223> OTHER INFORMATION: Amplification primer.
137 <400> SEQUENCE: 8
E--> 138 gggcggaaagc ttgaaggagg tatttaagga gaaaataccg catcagg
139 47
142 <210> SEQ ID NO: 9
143 <211> LENGTH: 44
144 <212> TYPE: DNA
145 <213> ORGANISM: Artificial Sequence
147 <220> FEATURE:
148 <221> NAME/KEY: misc_feature
149 <222> LOCATION: ()..()
150 <223> OTHER INFORMATION: Amplification primer.
154 <400> SEQUENCE: 9
E--> 155 gcccggtctc gagcgtctgt ttacaccat cgccttccc aaca
156 44
159 <210> SEQ ID NO: 10
160 <211> LENGTH: 47
161 <212> TYPE: DNA
162 <213> ORGANISM: Artificial Sequence
164 <220> FEATURE:
165 <221> NAME/KEY: misc_feature
166 <222> LOCATION: ()..()
167 <223> OTHER INFORMATION: Amplification primer.
169 <400> SEQUENCE: 10
E--> 170 gcccggtctc gagcgtctgt ttaaattcac tggccgtcgt tttacaa
171 47
174 <210> SEQ ID NO: 11
175 <211> LENGTH: 45
176 <212> TYPE: DNA
177 <213> ORGANISM: Artificial Sequence
W--> 179 <220> FEATURE:
W--> 179 <223> OTHER INFORMATION:
179 <400> SEQUENCE: 11
E--> 180 gcccggtctc gagcgtctgt ttaccaatac gcaaaccgcc tctcc
181 45
184 <210> SEQ ID NO: 12
185 <211> LENGTH: 48
186 <212> TYPE: DNA
187 <213> ORGANISM: Artificial Sequence
189 <220> FEATURE:
190 <221> NAME/KEY: misc_feature
191 <222> LOCATION: ()..()
192 <223> OTHER INFORMATION: Amplification primer.
195 <400> SEQUENCE: 12
E--> 196 ccactacgcc tccgctttcc tctcgccgg aagcttgaag gaggtatt

RAW SEQUENCE LISTING
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TIME: 17:34:54

Input Set : A:\SeqList.txt
Output Set: N:\CRF3\09212001\I767764.raw

197 48
200 <210> SEQ ID NO: 13
201 <211> LENGTH: 46
202 <212> TYPE: DNA
203 <213> ORGANISM: Artificial Sequence
205 <220> FEATURE:
206 <221> NAME/KEY: misc_feature
207 <222> LOCATION: ()..()
208 <223> OTHER INFORMATION: Amplification primer.
210 <400> SEQUENCE: 13
E--> 211 ctgccccggg ttccttcattc tctgcccgtt ctcgagcgta tgttta
212 46
215 <210> SEQ ID NO: 14
216 <211> LENGTH: 10
217 <212> TYPE: DNA
218 <213> ORGANISM: Artificial Sequence
220 <220> FEATURE:
221 <221> NAME/KEY: misc_feature
222 <222> LOCATION: ()..()
223 <223> OTHER INFORMATION: Oligonucleotide for array templating.
225 <400> SEQUENCE: 14
E--> 226 tgcatgctat
227 10
230 <210> SEQ ID NO: 15
231 <211> LENGTH: 25
232 <212> TYPE: DNA
233 <213> ORGANISM: Artificial Sequence
235 <220> FEATURE:
236 <221> NAME/KEY: misc_feature
237 <222> LOCATION: ()..()
238 <223> OTHER INFORMATION: Oligonucleotide for array templating.
243 <400> SEQUENCE: 15
E--> 244 cgatgcattt acgtaacgtt cgata
245 25
248 <210> SEQ ID NO: 16
249 <211> LENGTH: 32
250 <212> TYPE: DNA
251 <213> ORGANISM: Artificial Sequence
253 <220> FEATURE:
254 <221> NAME/KEY: misc_feature
255 <222> LOCATION: ()..()
256 <223> OTHER INFORMATION: Primer for in-situ amplification.
258 <220> FEATURE:
259 <221> NAME/KEY: misc_feature
260 <222> LOCATION: (27)..(32)<223> N can be a, c, g, or t.
262 <400> SEQUENCE: 16
E--> 263 gcagcagtagac gactagcata tccgacnnnn nn
264 32
267 <210> SEQ ID NO: 17

RAW SEQUENCE LISTING
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Input Set : A:\SeqList.txt
Output Set: N:\CRF3\09212001\I767764.raw

268 <211> LENGTH: 32
269 <212> TYPE: DNA
270 <213> ORGANISM: Artificial Sequence
272 <220> FEATURE:
273 <221> NAME/KEY: misc_feature
274 <222> LOCATION: ()..()
275 <223> OTHER INFORMATION: Primer for in-situ amplification.
277 <220> FEATURE:
278 <221> NAME/KEY: misc_feature
279 <222> LOCATION: (27)..(32)
280 <223> OTHER INFORMATION: N can be a, c, g, or t.
282 <400> SEQUENCE: 17
E--> 283 cgatagcagt agcatgcagg tccgacnnnn nn
284 32
286 <210> SEQ ID NO: 18
287 <211> LENGTH: 66
288 <212> TYPE: DNA
289 <213> ORGANISM: Artificial Sequence
291 <220> FEATURE:
292 <221> NAME/KEY: misc_feature
293 <222> LOCATION: ()..()
294 <223> OTHER INFORMATION: Prophetic example of genomic DNA sequence.
296 <400> SEQUENCE: 18
E--> 297 tcggctcatc tgcatgctgc cagcagtcgg actacgtacc ccggtagctg cgctacacgc
298 60
E--> 300 agcttt
301 66
304 <210> SEQ ID NO: 19
305 <211> LENGTH: 88
306 <212> TYPE: DNA
307 <213> ORGANISM: Artificial sequence
W--> 308 <220> FEATURE:
309 <221> NAME/KEY: misc_feature
310 <222> LOCATION: ()..()
311 <223> OTHER INFORMATION: Primer for in-situ amplification.
313 <400> SEQUENCE: 19
E--> 314 gcagcagtagcactacgactacata tccgacactgc gtgttagcgca cgtaccgggg tacgttagtcc
315 60
E--> 317 gactgctggc agcatgcaga tgagccga
318 88
321 <210> SEQ ID NO: 20
322 <211> LENGTH: 94
323 <212> TYPE: DNA
324 <213> ORGANISM: Artificial Sequence
326 <220> FEATURE:
327 <221> NAME/KEY: misc_feature
328 <222> LOCATION: ()..()
329 <223> OTHER INFORMATION: Primer for in-situ hybridization.
332 <400> SEQUENCE: 20

RAW SEQUENCE LISTING
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Input Set : A:\SeqList.txt
Output Set: N:\CRF3\09212001\I767764.raw

E--> 333 cgatagcagt agcatgcagg tccgaccagc agtcggacta cgtaccccggtacgtgcgt
334 60
E--> 336 acacgcaggt cggatatgct agtcgtactg ctgc
337 94
339 <210> SEQ ID NO: 21
340 <211> LENGTH: 94
341 <212> TYPE: DNA
342 <213> ORGANISM: Artificial Sequence
344 <220> FEATURE:
345 <221> NAME/KEY: misc_feature
346 <222> LOCATION: ()..()
347 <223> OTHER INFORMATION: Primer for in-situ hybridization.
349 <400> SEQUENCE: 21
E--> 350 gcagcagttac gactagcata tccgacctgc gtgttagcgca cgtaccgggg tacgttagtcc
351 60
E--> 353 gactgctggt cggacctgca tgctactgct atcg
354 94

VERIFICATION SUMMARY
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Input Set : A:\SeqList.txt
Output Set: N:\CRF3\09212001\I767764.raw

L:9 M:270 C: Current Application Number differs, Replaced Current Application No
L:9 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:23 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:17 SEQ:1
M:254 Repeated in SeqNo=1
L:24 M:252 E: No. of Seq. differs, <211>LENGTH:Input:24 Found:17 SEQ:1
L:38 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:24 SEQ:2
L:54 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:23 SEQ:3
L:69 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:4
L:73 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:24 SEQ:4
L:88 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:24 SEQ:5
L:103 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:23 SEQ:6
L:123 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:24 SEQ:7
L:138 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:47 SEQ:8
L:155 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:44 SEQ:9
L:170 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:47 SEQ:10
L:179 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:179 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:180 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:45 SEQ:11
L:196 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:48 SEQ:12
L:211 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:46 SEQ:13
L:226 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:10 SEQ:14
L:244 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:25 SEQ:15
L:263 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:16
L:263 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:32 SEQ:16
L:283 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:17
L:283 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:32 SEQ:17
L:297 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:60 SEQ:18
M:254 Repeated in SeqNo=18
L:308 M:283 W: Missing Blank Line separator, <220> field identifier
L:314 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:60 SEQ:19
M:254 Repeated in SeqNo=19
L:333 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:60 SEQ:20
M:254 Repeated in SeqNo=20
L:350 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:60 SEQ:21
M:254 Repeated in SeqNo=21